

RAW SEQUENCE LISTING

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Application Serial Number: 10/518,223A
Source: IFW/b
Date Processed by STIC: 9/1/06

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IFW16

RAW SEQUENCE LISTING

DATE: 09/01/2006

PATENT APPLICATION: US/10/518,223A

TIME: 10:48:14

Input Set : F:\00007135 030b-SEQ Listing from KMOB.TXT

Output Set: N:\CRF4\09012006\J518223A.raw

4 <110> APPLICANT: Cheng, Ning Man
5 Leung, Yun Chung
6 Lo, Wai Hung
8 <120> TITLE OF INVENTION: PHARMACEUTICAL PREPARATION AND METHOD OF
9 TREATMENT OF HUMAN MALIGNANCIES WITH ARGININE DEPRIVATION
12 <130> FILE REFERENCE: B001.001.NPRUS
14 <140> CURRENT APPLICATION NUMBER: 10/518,223A
15 <141> CURRENT FILING DATE: 2004-12-15
17 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/002665
18 <151> PRIOR FILING DATE: 2003-06-20
20 <150> PRIOR APPLICATION NUMBER: PCT/CN02/00635
21 <151> PRIOR FILING DATE: 2002-09-09
23 <150> PRIOR APPLICATION NUMBER: 60/390,757
24 <151> PRIOR FILING DATE: 2002-06-20
26 <160> NUMBER OF SEQ ID NOS: 9
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2002
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 1
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37 aagtgaagt cgagggaagt ccaagaaatg gtgattatga ggggtgtctat ttcacacaaa 120
38 acggagaata tttattggaa ttaagagtct ctgggactgc tcttgtaaata gctccttgta 180
39 atttaaagga tattgacata acgaaatggt tgtgtaaaac agggagatta tatcttgata 240
40 aggttaagaa atttgaaata gttactattc tttcccatga cgtagaaaat caaaagatta 300
41 taacagaatg ggagtcactc cccagagagg ctttaccgga acaatttgat tcataagaac 360
42 taattagtag cgctttccaa tggaggcgct tttttatttg ggtagttgca taccactaaa 420
43 gatgttcagg tgcacatgag cattggagga aaggaacgct ttagggggaa gggaaacctt 480
44 taaacagtct taatccccct tgattttatg ttctctgtaa actgctccg gtaaactctca 540
45 ggatagacaa tcggcggtta acggcttgag tgcgggggca gtttagaaag aatatgattg 600
46 gagggattca tagatgcata accatcacca tcatatgagc gccaaagtcca gaaccatagg 660
47 gattattgga gctcctttct caaagggaca gccacgagga ggggtggaag aaggccctac 720
48 agtattgaga aaggctggtc tgcttgagaa acttaaagaa caagagtgtg atgtgaagga 780
49 ttatggggac ctgccctttg ctgacatccc taatgacagt ccctttcaaa ttgtgaagaa 840
50 tccaaggtct gtgggaaaag caagcgagca gctggctggc aagggtggc aagtcagaa 900
51 gaacggaaga atcagcctgg tgctggcgcg agaccacagt ttggcaattg gaagcatctc 960
52 tggccatgcc agggctccacc ctgatcttgg agtcatctgg gtggatgctc aactgatata 1020
53 caacactcca ctgacaacca caagtggaaa cttgcatgga caacctgtat ctttctctct 1080
54 gaaggaaact aaaggaaaga ttcccgatgt gccaggattc tcctgggtga ctccctgtat 1140
55 atctgccaag gatattgtgt atattggctt gagagacgtg gacctgggg aacactacat 1200
56 tttgaaaact ctaggacatta aatacttttc aatgactgaa gtggacagac taggaattgg 1260
57 caaggtgatg gaagaaacac tcagctatct actaggaaga aagaaaaggc caattcatct 1320

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58 aagttttgat gttgacggac tggacccatc tttcacacca gctactggca caccagtcgt 1380
59 gggaggtctg acatacagag aaggtctcta catcacagaa gaaatctaca aaacagggct 1440
60 actctcagga ttagatataa tggaagtga cccatccctg gggaagacac cagaagaagt 1500
61 aactcgaaca gtgaacacag cagttgcaat aaccttggct tgtttcggac ttgctcggga 1560
62 gggtaatcac aagcctattg actaccttaa cccacctaa taaatgtgga aacatccgat 1620
63 ataaatctca tagttaatgg cataattaga aagctaata ttttcttaag catagagtta 1680
64 tccttctaaa gacttggtct ttcagaaaaa tgtttttcca attagtataa actctacaaa 1740
65 ttccctcttg gtgtaaaatt caagatgtgg aaattctaac ttttttgaaa tttaaaagct 1800
66 tatattttct aacttggcaa aagacttatc cttagaaaga gaagtgtaca ttgatttcca 1860
67 attaaaaatt tgctggcatt aaaaataagc acacttacat aagcccccat acatagagtg 1920
68 ggactcttgg aatcaggaga caaagctacc acatgtggaa aggtactatg tgtccatgtc 1980
69 attcaaaaaa tgtgattcta ga                                     2002

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71 <210> SEQ ID NO: 2

72 <211> LENGTH: 990

73 <212> TYPE: DNA

74 <213> ORGANISM: Artificial Sequence

76 <220> FEATURE:

77 <223> OTHER INFORMATION: Chimeric DNA sequence encoding human arginase I
 78 and an N-terminal histidine tag

80 <400> SEQUENCE: 2

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81 atg cat cac cat cac cat cat atg agc gcc aag tcc aga acc ata ggg 48
82 att att gga gct cct ttc tca aag gga cag cca cga gga ggg gtg gaa 96
83 gaa ggc cct aca gta ttg aga aag gct ggt ctg ctt gag aaa ctt aaa 144
84 gaa caa gag tgt gat gtg aag gat tat ggg gac ctg ccc ttt gct gac 192
85 atc cct aat gac agt ccc ttt caa att gtg aag aat cca agg tct gtg 240
86 gga aaa gca agc gag cag ctg gct ggc aag gtg gca caa gtc aag aag 288
87 aac gga aga atc agc ctg gtg ctg ggc gga gac cac agt ttg gca att 336
88 gga agc atc tct ggc cat gcc agg gtc cac cct gat ctt gga gtc atc 384
89 tgg gtg gat gct cac act gat atc aac act cca ctg aca acc aca agt 432
90 gga aac ttg cat gga caa cct gta tct ttc ctg aag gaa cta aaa 480
91 gga aag att ccc gat gtg cca gga ttc tcc tgg gtg act ccc tgt ata 528
92 tct gcc aag gat att gtg tat att ggc ttg aga gac gtg gac cct ggg 576
93 gaa cac tac att ttg aaa act cta ggc att aaa tac ttt tca atg act 624
94 gaa gtg gac aga cta gga att ggc aag gtg atg gaa gaa aca ctc agc 672
95 tat cta cta gga aga aag aaa agg cca att cat cta agt ttt gat gtt 720
96 gac gga ctg gac cca tct ttc aca cca gct act ggc aca cca gtc gtg 768
97 gga ggt ctg aca tac aga gaa ggt ctc tac atc aca gaa gaa atc tac 816
98 aaa aca ggg cta ctc tca gga tta gat ata atg gaa gtg aac cca tcc 864
99 ctg ggg aag aca cca gaa gaa gta act cga aca gtg aac aca gca gtt 912
100 gca ata acc ttg gct tgt ttc gga ctt gct cgg gag ggt aat cac aag 960
101 cct att gac tac ctt aac cca cct aag taa 990

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103 <210> SEQ ID NO: 3

104 <211> LENGTH: 329

105 <212> TYPE: PRT

106 <213> ORGANISM: Artificial Sequence

108 <220> FEATURE:

109 <223> OTHER INFORMATION: Chimeric AA sequence of human arginase I and an
 110 N-terminal histidine tag

112 <400> SEQUENCE: 3

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113 Met His His His His His His Met Ser Ala Lys Ser Arg Thr Ile Gly
114 1 5 10 15
115 Ile Ile Gly Ala Pro Phe Ser Lys Gly Gln Pro Arg Gly Gly Val Glu
116 20 25 30
117 Glu Gly Pro Thr Val Leu Arg Lys Ala Gly Leu Leu Glu Lys Leu Lys
118 35 40 45
119 Glu Gln Glu Cys Asp Val Lys Asp Tyr Gly Asp Leu Pro Phe Ala Asp
120 50 55 60
121 Ile Pro Asn Asp Ser Pro Phe Gln Ile Val Lys Asn Pro Arg Ser Val
122 65 70 75 80
123 Gly Lys Ala Ser Glu Gln Leu Ala Gly Lys Val Ala Gln Val Lys Lys
124 85 90 95
125 Asn Gly Arg Ile Ser Leu Val Leu Gly Asp His Ser Leu Ala Ile
126 100 105 110
127 Gly Ser Ile Ser Gly His Ala Arg Val His Pro Asp Leu Gly Val Ile
128 115 120 125
129 Trp Val Asp Ala His Thr Asp Ile Asn Thr Pro Leu Thr Thr Thr Ser
130 130 135 140
131 Gly Asn Leu His Gly Gln Pro Val Ser Phe Leu Leu Lys Glu Leu Lys
132 145 150 155 160
133 Gly Lys Ile Pro Asp Val Pro Gly Phe Ser Trp Val Thr Pro Cys Ile
134 165 170 175
135 Ser Ala Lys Asp Ile Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Gly
136 180 185 190
137 Glu His Tyr Ile Leu Lys Thr Leu Gly Ile Lys Tyr Phe Ser Met Thr
138 195 200 205
139 Glu Val Asp Arg Leu Gly Ile Gly Lys Val Met Glu Glu Thr Leu Ser
140 210 215 220
141 Tyr Leu Leu Gly Arg Lys Lys Arg Pro Ile His Leu Ser Phe Asp Val
142 225 230 235 240
143 Asp Gly Leu Asp Pro Ser Phe Thr Pro Ala Thr Gly Thr Pro Val Val
144 245 250 255
145 Gly Gly Leu Thr Tyr Arg Glu Gly Leu Tyr Ile Thr Glu Glu Ile Tyr
146 260 265 270
147 Lys Thr Gly Leu Leu Ser Gly Leu Asp Ile Met Glu Val Asn Pro Ser
148 275 280 285
149 Leu Gly Lys Thr Pro Glu Glu Val Thr Arg Thr Val Asn Thr Ala Val
150 290 295 300
151 Ala Ile Thr Leu Ala Cys Phe Gly Leu Ala Arg Glu Gly Asn His Lys
152 305 310 315 320
153 Pro Ile Asp Tyr Leu Asn Pro Pro Lys
154 325
157 <210> SEQ ID NO: 4
158 <211> LENGTH: 7
159 <212> TYPE: PRT
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: 6x Histidine tag
165 <400> SEQUENCE: 4

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Output Set: N:\CRF4\09012006\J518223A.raw

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166 Met His His His His His His
167 1 5
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 33
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
178 <400> SEQUENCE: 5
179 ccaaaccata tgagcgccaa gtccagaacc ata 33
181 <210> SEQ ID NO: 6
182 <211> LENGTH: 39
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
189 <400> SEQUENCE: 6
190 ccaaactcta gaatcacatt ttttgaatga catggacac 39
192 <210> SEQ ID NO: 7
193 <211> LENGTH: 24
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
200 <400> SEQUENCE: 7
201 ctctggccat gccagggtcc accc 24
203 <210> SEQ ID NO: 8
204 <211> LENGTH: 969
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)...(969)
212 <400> SEQUENCE: 8
213 atg agc gcc aag tcc aga acc ata ggg att att gga gct cct ttc tca 48
214 Met Ser Ala Lys Ser Arg Thr Ile Gly Ile Ile Gly Ala Pro Phe Ser
215 1 5 10 15
217 aag gga cag cca cga gga ggg gtg gaa gaa ggc cct aca gta ttg aga 96
218 Lys Gly Gln Pro Arg Gly Gly Val Glu Glu Gly Pro Thr Val Leu Arg
219 20 25 30
221 aag gct ggt ctg ctt gag aaa ctt aaa gaa caa gag tgt gat gtg aag 144
222 Lys Ala Gly Leu Leu Glu Lys Leu Lys Glu Gln Glu Cys Asp Val Lys
223 35 40 45
225 gat tat ggg gac ctg ccc ttt gct gac atc cct aat gac agt ccc ttt 192
226 Asp Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe
227 50 55 60
229 caa att gtg aag aat cca agg tct gtg gga aaa gca agc gag cag ctg 240
230 Gln Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu
231 65 70 75 80

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233 gct ggc aag gtg gca caa gtc aag aag aac gga aga atc agc ctg gtg 288
234 Ala Gly Lys Val Ala Gln Val Lys Lys Asn Gly Arg Ile Ser Leu Val
235      85      90      95
237 ctg ggc gga gac cac agt ttg gca att gga agc atc tct ggc cat gcc 336
238 Leu Gly Gly Asp His Ser Leu Ala Ile Gly Ser Ile Ser Gly His Ala
239      100      105      110
241 agg gtc cac cct gat ctt gga gtc atc tgg gtg gat gct cac act gat 384
242 Arg Val His Pro Asp Leu Gly Val Ile Trp Val Asp Ala His Thr Asp
243      115      120      125
245 atc aac act cca ctg aca acc aca agt gga aac ttg cat gga caa cct 432
246 Ile Asn Thr Pro Leu Thr Thr Thr Ser Gly Asn Leu His Gly Gln Pro
247      130      135      140
249 gta tct ttc ctc ctg aag gaa cta aaa gga aag att ccc gat gtg cca 480
250 Val Ser Phe Leu Leu Lys Glu Leu Lys Gly Lys Ile Pro Asp Val Pro
251 145      150      155      160
253 gga ttc tcc tgg gtg act ccc tgt ata tct gcc aag gat att gtg tat 528
254 Gly Phe Ser Trp Val Thr Pro Cys Ile Ser Ala Lys Asp Ile Val Tyr
255      165      170      175
257 att ggc ttg aga gac gtg gac cct ggg gaa cac tac att ttg aaa act 576
258 Ile Gly Leu Arg Asp Val Asp Pro Gly Glu His Tyr Ile Leu Lys Thr
259      180      185      190
261 cta ggc att aaa tac ttt tca atg act gaa gtg gac aga cta gga att 624
262 Leu Gly Ile Lys Tyr Phe Ser Met Thr Glu Val Asp Arg Leu Gly Ile
263      195      200      205
265 ggc aag gtg atg gaa gaa aca ctc agc tat cta cta gga aga aag aaa 672
266 Gly Lys Val Met Glu Glu Thr Leu Ser Tyr Leu Leu Gly Arg Lys Lys
267      210      215      220
269 agg cca att cat cta agt ttt gat gtt gac gga ctg gac cca tct ttc 720
270 Arg Pro Ile His Leu Ser Phe Asp Val Asp Gly Leu Asp Pro Ser Phe
271 225      230      235      240
273 aca cca gct act ggc aca cca gtc gtg gga ggt ctg aca tac aga gaa 768
274 Thr Pro Ala Thr Gly Thr Pro Val Val Gly Gly Leu Thr Tyr Arg Glu
275      245      250      255
277 ggt ctc tac atc aca gaa gaa atc tac aaa aca ggg cta ctc tca gga 816
278 Gly Leu Tyr Ile Thr Glu Glu Ile Tyr Lys Thr Gly Leu Leu Ser Gly
279      260      265      270
281 tta gat ata atg gaa gtg aac cca tcc ctg ggg aag aca cca gaa gaa 864
282 Leu Asp Ile Met Glu Val Asn Pro Ser Leu Gly Lys Thr Pro Glu Glu
283      275      280      285
285 gta act cga aca gtg aac aca gca gtt gca ata acc ttg gct tgt ttc 912
286 Val Thr Arg Thr Val Asn Thr Ala Val Ala Ile Thr Leu Ala Cys Phe
287      290      295      300
289 gga ctt gct cgg gag ggt aat cac aag cct att gac tac ctt aac cca 960
290 Gly Leu Ala Arg Glu Gly Asn His Lys Pro Ile Asp Tyr Leu Asn Pro
291 305      310      315      320
293 cct aag taa 969
294 Pro Lys *
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 322

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VERIFICATION SUMMARY

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